

## SEQUENCE LISTING

<110> Japan Science and Technology Corporation  
manager of Natinal Insutitute of Infectious Diseases

<120> Medicine for promoting ceramide transportation, sequence for manufacturing the medicine, method for measuring the promoting activity for ceramide isolation, and method for measuring the promoting activity for ceramide migration between membranes

<130> P000

<160> 32

<170> PatentIn version 3.1

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Trp Thr Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys  
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Asn Asn Ala Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly  
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Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp  
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Phe Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr  
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Leu Arg Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile

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Asp Val Gly Gly Asp Ala Asn Trp Gln Leu Val Val Glu Glu Gly Glu  
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Cys Asn Tyr Phe Trp Asn Val Asp Val Arg Asn Asp Trp Glu Thr Thr  
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Ile Glu Asn Phe His Val Val Glu Thr Leu Ala Asp Asn Ala Ile Ile  
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Ile Tyr Gln Thr His Lys Arg Val Trp Pro Ala Ser Gln Arg Asp Val  
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Leu Tyr Leu Ser Val Ile Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp

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Pro Glu Thr Trp Ile Val Cys Asn Phe Ser Val Asp His Asp Ser Ala  
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Pro Leu Asn Asn Arg Cys Val Arg Ala Lys Ile Asn Val Ala Met Ile  
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Cys Gln Thr Leu Val Ser Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg  
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Asp Asn Ile Leu Cys Lys Ile Thr Tyr Val Ala Asn Val Asn Pro Gly  
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Gly Trp Ala Pro Ala Ser Val Leu Arg Ala Val Ala Lys Arg Glu Tyr  
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Asn Asn Ala Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly  
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Phe Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr  
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Leu Arg Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile  
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Glu Gln His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg  
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Arg His Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser  
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Ala Thr Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys  
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Thr Leu Gln Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp  
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Glu Leu Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro  
195 200 205

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Glu Lys Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp  
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Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu  
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Trp Gln Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu  
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Glu Phe Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile  
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Leu Pro Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val  
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Gln Lys Pro Tyr Ser Arg Ser Ser Ser Met Ser Ser Ile Asp Leu Val  
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Val Glu Thr Leu Ala Asp Asn Ala Ile Ile Ile Tyr Gln Thr His Lys  
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Arg Val Trp Pro Ala Ser Gln Arg Asp Val Leu Tyr Leu Ser Val Ile  
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Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp Pro Glu Thr Trp Ile Val  
515 520 525

Cys Asn Phe Ser Val Asp His Asp Ser Ala Pro Leu Asn Asn Arg Cys  
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Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg Asp Asn Ile Leu Cys Lys  
565 570 575

Ile Thr Tyr Val Ala Asn Val Asn Pro Gly Gly Trp Ala Pro Ala Ser  
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Asn Asn Thr Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly  
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Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp  
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Phe Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr  
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Leu Arg Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile  
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Glu Gln His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg  
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Thr Leu Gln Lys Tyr Phe Asp Val Cys Ala Asp Ala Val Ser Lys Asp  
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Glu Leu Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro  
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Glu Lys Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp  
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Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu  
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Trp Gln Lys Arg His Asp Lys Glu Met Glu Lys Arg Arg Arg Leu Glu  
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Glu Ala Tyr Lys Asn Ala Met Ala Glu Leu Lys Lys Lys Pro Arg Phe  
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Gly Gly Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu  
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Glu Phe Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile  
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Glu Glu Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Pro  
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Leu Pro Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val  
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Gln Lys Val Glu Glu Met Val Gln Asn His Met Thr Tyr Ser Leu Gln  
370 375 380

Asp Val Gly Gly Asp Ala Asn Trp Gln Leu Val Val Glu Glu Gly Glu  
385 390 395 400

Met Lys Val Tyr Arg Arg Glu Val Glu Glu Asn Gly Ile Val Leu Asp  
405 410 415

Pro Leu Lys Ala Thr His Ala Val Lys Gly Val Thr Gly His Glu Val  
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Cys Asn Tyr Phe Trp Ser Val Asp Val Arg Asn Asp Trp Glu Thr Thr  
435 440 445

Ile Glu Asn Phe His Val Val Glu Thr Leu Ala Asp Asn Ala Ile Ile  
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Ile Tyr Gln Thr His Lys Arg Val Trp Pro Ala Ser Gln Arg Asp Val  
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Leu Tyr Leu Ser Ala Ile Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp  
485 490 495

Pro Glu Thr Trp Ile Val Cys Asn Phe Ser Val Asp His Asp Ser Ala  
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Pro Leu Asn Asn Arg Cys Val Arg Ala Lys Ile Asn Val Ala Met Ile  
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Cys Gln Thr Leu Val Ser Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg  
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Asp Asn Ile Leu Cys Lys Ile Thr Tyr Val Ala Asn Val Asn Pro Gly  
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Gly Trp Ala Pro Ala Ser Val Leu Arg Ala Val Ala Lys Arg Glu Tyr  
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Asn Asn Thr Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly  
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Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp  
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Phe Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr  
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Leu Arg Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile  
 100 105 110

Glu Gln His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg  
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Arg His Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser  
 130 135 140

Ala Thr Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys  
 145 150 155 160

Leu Ala Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp  
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Thr Leu Gln Lys Tyr Phe Asp Val Cys Ala Asp Ala Val Ser Lys Asp  
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Glu Leu Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro  
 195 200 205

Thr Thr Arg Ser Asp Gly Asp Phe Leu His Asn Thr Asn Gly Asn Lys  
 210 215 220

Glu Lys Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp  
 225 230 235 240

Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu  
 245 250 255

Ala Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Glu Ser  
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Trp Gln Lys Arg His Asp Lys Glu Met Glu Lys Arg Arg Arg Leu Glu  
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Glu Ala Tyr Lys Asn Ala Met Ala Glu Leu Lys Lys Lys Pro Arg Phe  
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Gly Gly Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu  
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Glu Phe Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile  
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Glu Glu Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Pro  
340 345 350

Leu Pro Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val  
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Gln Lys Pro Tyr Ser Arg Ser Ser Ser Met Ser Ser Ile Asp Leu Val  
370 375 380

Ser Ala Ser Asp Asp Val His Arg Phe Ser Ser Gln Val Glu Glu Met  
385 390 395 400

Val Gln Asn His Met Thr Tyr Ser Leu Gln Asp Val Gly Gly Asp Ala  
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Asn Trp Gln Leu Val Val Glu Glu Gly Glu Met Lys Val Tyr Arg Arg  
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Glu Val Glu Glu Asn Gly Ile Val Leu Asp Pro Leu Lys Ala Thr His  
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Ala Val Lys Gly Val Thr Gly His Glu Val Cys Asn Tyr Phe Trp Ser  
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Val Asp Val Arg Asn Asp Trp Glu Thr Thr Ile Glu Asn Phe His Val  
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Val Glu Thr Leu Ala Asp Asn Ala Ile Ile Ile Tyr Gln Thr His Lys  
485 490 495

Arg Val Trp Pro Ala Ser Gln Arg Asp Val Leu Tyr Leu Ser Ala Ile  
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Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp Pro Glu Thr Trp Ile Val  
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Cys Asn Phe Ser Val Asp His Asp Ser Ala Pro Leu Asn Asn Arg Cys  
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Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg Asp Asn Ile Leu Cys Lys  
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Ile Thr Tyr Val Ala Asn Val Asn Pro Gly Gly Trp Ala Pro Ala Ser  
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1320

agcttaagaa gaaaccccg tttggagggc ctgattatga agaaggctcg aacagtctga  
1380

ttaatgagga ggagttcttt gatgctgttg aagctgctct tgacagacaa gataaaatag  
1440

aggaacagtc acagagcgag aaggtcaggt tacactggcc tacacctttg ccatctggag  
1500

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atgccttttc ttctgttggg acccatagat ttgtacaaaa ggttgaagag atggtacaga  
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1620

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ctttgaaagc taccatgca gttaaagggtg ttacaggaca cgaagtctgc aattactttt  
1740

ggagtgttga tgttcgcaat gactgggaaa ctactataga aaacttccat gtagtgga  
1800

cattagctga taatgcaatc atcatttate aaacgcacaa gagagtgtgg cctgcttctc  
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1920

ctgagacttg gatagtttgt aatttttctg tggatcatga cagcgctcct ctgaacaatc  
1980

gatgtgtccg tgccaaaate aatgttgcta tgatttgtca aaccttagta agcccaccag  
2040

agggaaacca ggaaataagc agagacaaca ttctgtgcaa gattacatat gtagctaattg  
2100

tgaacccagg aggatgggca ccagcctcgg tgtaagagc agtggcaaaa cgagaatatc  
2160

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2220

tgtttttagta tgtacagtga ctgaagcaag gctgtgtgac attccatggt ggagaaagaa  
2280

agaagaaaaa ttgagttctc taagctggaa cataggatct acagccttgt ccatggccca  
2340

agaagaatca ttgcaatagt aaagctgggt atctaact agccatctcc tgatagatct  
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180

acagagtacg gttgcagggg atccatctgt cttagcaagg ctgtgatcac acctcatgat  
240

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300

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tatggatctg agtccagctt acgtagacat ggctcaatgg tgtcactggg gtctggagca  
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agtgggtact ctgctacatc cacatcttca ttcaagaaag gacacagttt acgtgagaaa  
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540

tactttgatg tctgtgctga tgctgtctcc aaggatgaac ttcaaaggga taaagtggta  
600

gaagatgatg aagatgactt ccctacaact cgttctgatg gagacttttt gcacaatacc  
660

aatggtaata aggaaaaatt atttccacat gtaaccccca aaggaattaa tggatatagac  
720

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780

cattgtattg aattaatggg aaaacgggaa gagagctggc aaaaaagaca tgataaggaa  
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1080

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1740

gctaattgta acccaggagg atgggcacca gcctcgggtg taagagcagt ggcaaaacga  
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56

<210> 13  
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<212> DNA

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<210> 22

<211> 38

<212> DNA

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<210> 23

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